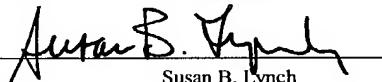


PATENT  
Docket No. 511582001601

CERTIFICATE OF MAILING BY "FIRST CLASS MAIL"

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Susan B. Lynch

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In the application of:

Daniel E. AFAR et al.

Serial No.: 10/010,667

Filing Date: 06 December 2001

For: PEPTIDES DERIVED FROM STEAP1  
(AS AMENDED)

Examiner: To be assigned

Group Art Unit: To be assigned

**RESPONSE TO NOTICE TO FILE CORRECTED APPLICATION PAPERS**

Box Sequence  
Assistant Commissioner for Patents  
P.O. Box 2327  
Arlington, VA 22202

Dear Sir:

This is in response to the Notice to file Corrected Application Papers of nonprovisional application 10/010,667 mailed January 29, 2002, for which a response is due on March 29, 2002. Accordingly, this response is timely filed.

Please enter the following Sequence Listing, amendments and remarks.

In the Sequence Listing:

Please insert the attached paper copy of the Sequence Listing as new pages 1-10 in the above-captioned application. A computer-readable form copy (CRF copy) of the Sequence Listing accompanies this response.

## AMENDMENTS

In the Specification

Please replace the paragraph beginning at page 5, line 35, with the following rewritten paragraph:

FIG. 4-1- 4-2. Nucleotide sequence of STEAP-1 GTH9 clone (SEQ ID NO:6) corresponding to the 4 kb message on northern blots (FIG. 3A). The sequence contains an intron of 2399 base pairs relative to the STEAP-1 clone 10 sequence of FIG. 1A; coding regions are nucleotides 96-857 and 3257-3510 (indicated in bold). The start ATG is in bold and underlined, the STOP codon is in bold and underlined, and the intron-exon boundaries are underlined.--

Please replace the paragraph beginning at page 7, line 23, with the following rewritten paragraph:

-- FIG. 11. Primary structural comparison of STEAP family proteins. FIG. 11A. Amino acid sequence alignment of STEAP-1 (8P1D4 CLONE 10; SEQ ID NO:2) and STEAP-2 (98P4B6;SEQ ID NO: 8) sequences. The alignment was performed using the SIM alignment program of the Baylor College of Medicine Search Launcher Web site. Results show a 61.4% identity in a 171 amino acid overlap; Score: 576.0; Gap frequency: 0.0%. FIG. 11B. Amino acid sequence alignment of STEAP-1 with partial ORF sequences of STEAP-2 and two other putative family member proteins using PIMA program (PIMA 1.4 program at Internet address <<http://dot.imgen.bcm.tmc.edu:9331/multi-align/multi-align.html>>); transmembrane domains identified by the SOSUI program (available at Internet address <[http://www.tuat.ac.jp/~mitaku/adv\\_sosui/submit.html](http://www.tuat.ac.jp/~mitaku/adv_sosui/submit.html)>). are in bold.--

Please replace the paragraph beginning at page 8, line 12, with the following rewritten paragraph:

--FIG. 14A-B. Predominant expression of STEAP-2 (98P4B6) in prostate tissue. First strand cDNA was prepared from 8 normal tissues, the LAPC xenografts (4AD, 4Al and 9AD) and HeLa cells. Normalization was performed by PCR using primers to actin and GAPDH. Semi-quantitative PCR, using primers to 98P4B6, shows predominant expression of 98P4B6 in normal prostate and the LAPC xenografts. The following primers were used to amplify STEAP II:

98P4B6.1 5'GACTGAGCTGGAACTGGAATTGT 3' (SEQ ID NO:17)

98P4B6.2 5' TTTGAGGAGACTTCATCTCACTGG 3' (SEQ ID NO:18)--

Please replace the paragraph beginning at page 37, line 25, with the following rewritten paragraph:

--Normalization of the first strand cDNAs from multiple tissues was performed by using the primers 5'atatccgcgcgtcgatcgacaa3' (SEQ ID NO:30) and 5'agccacacgcagcttgcattgttagagg 3' (SEQ ID NO:31) to amplify  $\beta$ -actin. First strand cDNA (5 $\mu$ l) was amplified in a total volume of 50 $\mu$ l containing 0.4 $\mu$ M primers, 0.2 $\mu$ M each dNTPs, 1XPCR buffer (Clontech, 10mM Tris-HCL, 1.5 mM MgCl<sub>2</sub>, 50 mM KCL, pH8.3) and 1X Klentaq DNA polymerase (Clontech). Five  $\mu$ l of the PCR reaction was removed at 18, 20, and 22 cycles and used for agarose gel electrophoresis. PCR was performed using an MJ Research thermal cycle under the following conditions: initial denaturation was at 94°C for 15 sec, followed by a 18, 20, and 22 cycles of 94°C for 15, 65°C for 2 min, 72°C for 5 sec. A final extension at 72°C was carried out for 2 min. After agarose gel electrophoresis, the band intensities of the 283 bp  $\beta$ -actin bands from multiple tissues were compared by visual inspection. Dilution factors for the first strand cDNAs were calculated to result in equal  $\beta$ -actin band intensities in all tissues after 22 cycles of PCR. Three rounds of normalization were required to achieve equal band intensities in all tissues after 22 cycles of PCR--

Please replace the paragraph beginning at page 42, line 10, with the following rewritten paragraph:

--Example 3D: Immunohistochemical Analysis of STEAP-1 Protein Expression in Prostate Tumor Biopsy and Surgical Specimens

To determine the extent of STEAP-1 protein expression in clinical materials, tissue sections were prepared from a variety of prostate cancer biopsies and surgical samples for immunohistochemical analysis. Tissues were fixed in 10% formalin, embedded in paraffin, and sectioned according to standard protocol. Formalin-fixed, paraffin-embedded sections of LNCaP cells were used as a positive control. Sections were stained with an anti-STEAP-1 polyclonal antibody directed against a STEAP-1 N-terminal epitope (as described immediately above). LNCaP sections were stained in the presence of an excess amount of the STEAP-1 N-terminal peptide immunogen used to generate the polyclonal antibody (peptide 1) or a non-specific peptide derived from a distinct region of the STEAP-1 protein (peptide 2; YQQVQQNKEDAWIEH). (SEQ ID NO:32)--

## REMARKS

The Specification has been amended to include SEQ ID numbers which were omitted at the time of filing.

Attached hereto is a marked-up version of the changes made to the specification by the current amendment. The attached page is captioned "Version with markings to show changes made.".

The undersigned hereby states that the paper copy Sequence Listing and the computer readable form copy (CRF copy) of the Sequence Listing, submitted in accordance with 37 C.F.R. § 1.825(a) and (b), respectively, are the same and contain no new matter. Accordingly, entry of the Sequence Listing into the above-captioned case is respectfully requested.

In the unlikely event that the transmittal letter is separated from this document and the Patent Office determines that an extension and/or other relief is required, applicant petitions for any required relief including extensions of time and authorizes the Assistant Commissioner to charge the cost of such petitions and/or other fees due in connection with the filing of this document to Deposit Account No. 03-1952 referencing docket no. 511582001601. However, the Assistant Commissioner is not authorized to charge the cost of the issue fee to the Deposit Account.

Respectfully submitted,

Dated: March 22, 2002

By:

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**Version with markings to show changes made**

**In the Specification:**

On page 5, line 35, after “FIG.4” insert --1 - 4-2--;

On page 7, line 24, after “SEQ ID NO:” insert --2--;

On page 7, line 25, after “SEQ ID NO:” insert --8--;

On page 8, line 12, after “FIG. 14” insert --A - B--;

On page 37, line 26, after “caa3”” insert --(SEQ ID NO:30)--;

On page 37, line 26, after “agg3”” insert --(SEQ ID NO:31)--;

On page 42, line 21, after “IEH).” insert --(SEQ ID NO:32)--.